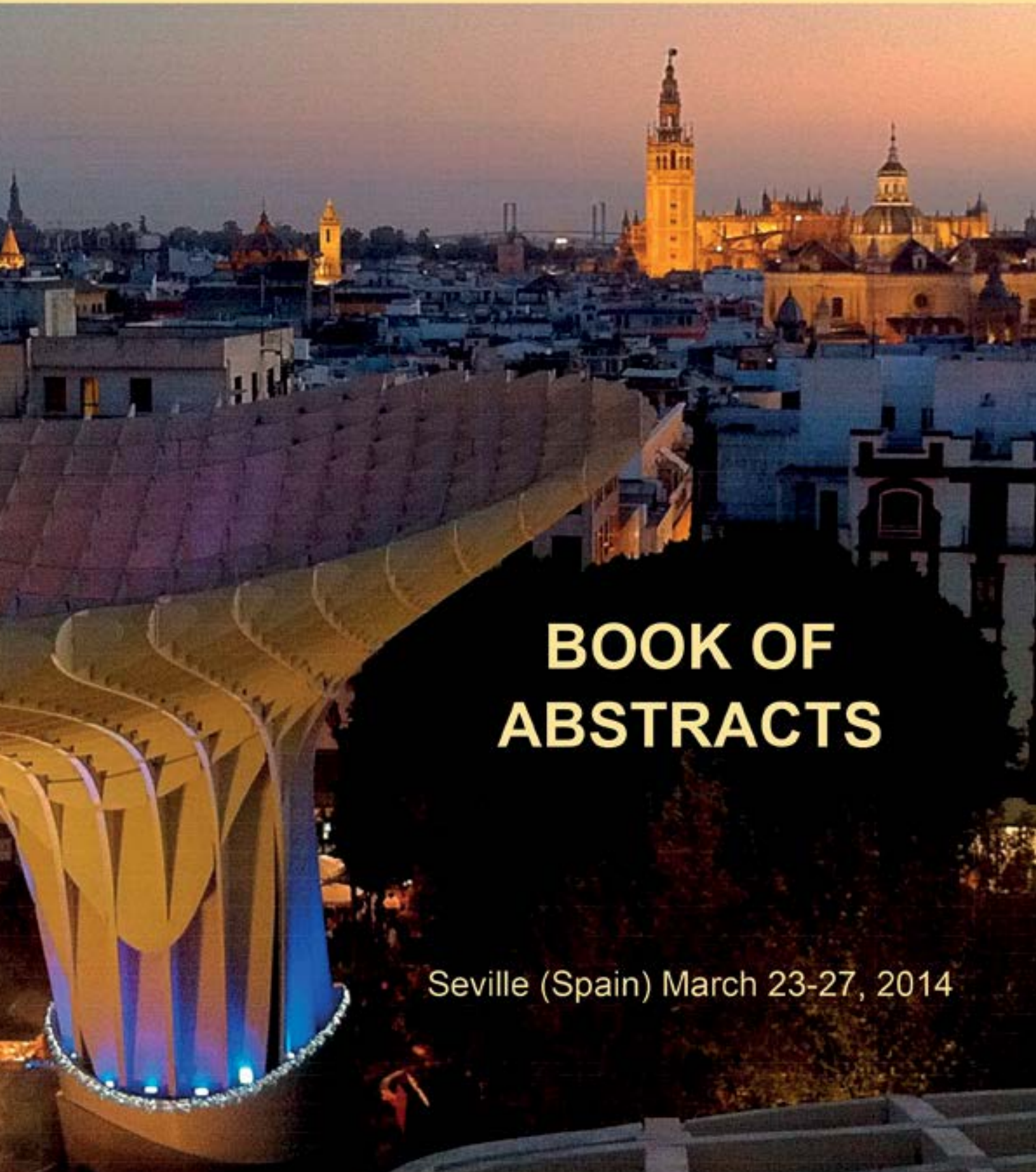
ECFG12
Seville 2014

12th European Conference on Fungal Genetics



BOOK OF ABSTRACTS

Seville (Spain) March 23-27, 2014

171 AN IN SILICO SEARCH FOR GLUCOSE-METHANOL-CHOLINE OXIDOREDUCTASES WITH INTERESTING FEATURES IN TEN POLYPORALES GENOMES

PATRICIA FERREIRA[1], **JUAN CARRO ARAMBURU**[2], ÁNGEL T. MARTÍNEZ[2]

[1] UNIVERSIDAD DE ZARAGOZA, SPAIN, [2] CIB-CSIC, SPAIN

The aim of this work was to find new glucose-methanol-choline (GMC) oxidoreductases with potential biotechnological applications taking advantage of the great deal of fungal genomes currently available. In order to do so, ten fungal species were selected (Bjerkandera adusta, Phlebia brevispora, Ganoderma sp., Fomitopsis pinicola, Phanerochaete chrysosporium, Dichomitus squalens, Ceriporiopsis subvermispora, Trametes versicolor, Rhodonia placenta and Wolfiporia cocos) from the order Polyporales, which possess the ability of degrading wood and, hence, have the degradative machinery encoded in their genomes. We performed an in silico search through protein sequence homology using cloned enzymes (aryl-alcohol oxidases, glucose oxidases, methanol oxidases, pyranose oxidases, cellobiose dehydrogenases and pyranose dehydrogenases) from related fungi. Once the putative enzymes of each class chosen, their sequences manually curated and annotated, we: i) analyzed their evolutionary relationships by constructing gene phylograms based on their predicted protein sequences; and ii) established their duplication/reduction history during fungal evolution by investigating the number of genes of each enzyme type most probably present at every node in the species evolutionary tree (by reconciliation between our constructed gene tree and the species tree available). Moreover, we modelled almost all the GMC sequences out of the 195 found in the ten genomes using the crystallographic structures of related enzymes as templates to gain insight into their structural variation and hypothesize their probable catalytic properties.

172 AN UPDATE OF ON-GOING WORK WITH CADRE AND ASPERCYC

JANE MABEY GILSENAN, PAUL BOWYER, MIKE BROMLEY

UNIVERSITY OF MANCHESTER, UNITED KINGDOM

The Central Aspergillus Data Resource (CADRE; www.cadre-genomes.org.uk) gathers automated and manual annotation efforts for this genus, providing enriched data for each genome. This information flows into AsperCyc (www.aspercyc.org.uk), an online resource of predicted metabolic pathways for the Aspergillus genus. Recently, much work has been going on that will filter into these online resources. We have recently been involved in an EC-FP7 funded systems biology study of fungal pathogens (Sybaris) during which we sequenced and annotated nine Aspergillus fumigatus strains, including CEA10 and AF300, and one A. nidulans strain (F8226) using data from CADRE. Currently, we are involved in another EC-FP7 funded project (NOFUN; www.nofunproject.org) that builds on our earlier work and aims to identify novel drug targets and to develop novel classes of antifungal drugs. Both projects have and will involve RNAseq analyses, data that we can make available, along with the strains, within CADRE.

ECFG12
Seville 2014

12th European Conference on Fungal Genetics

Seville (Spain) March 23-27, 2014

Institutional sponsors

Private sponsors

Poster awards sponsors